



# SEQUENCE LISTING

<110> MARINE BIOTECHNOLOGY INSTITUTE CO., LTD.  
Yasuhiro NISHIDA et al.

<120> NOVEL CAROTENOID HYDROXYLASE GENE, METHOD FOR PREPARING HYDROXYLATED  
CAROTENOID, AND NOVEL GERANYLGERANYL PYROPHOSHATE SYNTHASE

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<140> US 10/579,338

<141> 2006-05-15

<150> JP 2003/388165

<151> 2003-11-26

<150> JP 2004/165919

<151> 2004-06-03

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<170> PatentIn Ver. 2.1

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 Ala Thr His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly  
 210 215 220

ctc tat ttc cag ttc tgg gac cgc tgg gcc ggg act gag gtt tcg gcc 11461  
 Leu Tyr Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala  
 225 230 235

gcc ccc tcg cca cca tcc ccg gtc atc cct cca gag cgg ccc tca gcg 11509  
 Ala Pro Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala  
 240 245 250

cct ctt cgg tgatcggcctt ggtcaggggcg ggcgtggggcg cccaggccgg 11558  
 Pro Leu Arg  
 255

tcgccatctg cagtatggac gacgaggcca gacgtcccc gccgctcatg gcgatgaccc 11618

gcagggagtc cctcaaatgc cgggtgtcca tgatgaagtt cagcccgtcg cggtcgggca 11678

tcagaatgtc caccagcacg gcgtcggggcg accagtcctc gacgatccgc aaccogtcgt 11738

tgaccgttgc tgcggtcagg acttggcaac ccagccgttt cagcatctcc tccagatgaa 11798

gcagaaccag cgaatcgtcc tcgatcacgc agactttcac gcccaacctc cagatgcgat 11858

cagggggaac taacggatga atcccatgtt gcgtcaactc ggaagacggc gtttccgact 11918

ggccatcgcc ttggcggggcg cggtcgtgac cctgcttctg gcggccactg gggtgacgct 11978

gcaacgagaa ttc 11991

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 <212> DNA  
 <213> Brevundimonas sp.

<220>  
 <221> CDS  
 <222> (1)..(771)

<400> 3  
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 Met Leu Arg Asp Leu Leu Ile Thr Thr Leu Ala Leu Ser Leu Ile Ile  
 1 5 10 15

ggc ctg cgc tat ctg ctg gtc ggc gcg gcg gcc cat ggg ctg ctg tgg 96  
 Gly Leu Arg Tyr Leu Leu Val Gly Ala Ala Ala His Gly Leu Leu Trp  
 20 25 30

gcc ggg gcg ggc cgg gga cgg gcg ctg aac ctg cgg ccg ccg gcg atg 144

Ala Gly Ala Gly Arg Gly Arg Ala Leu Asn Leu Arg Pro Pro Ala Met	
35 40 45	
aag cgc atc cgc gcc gag atc gtc gcc tcc ctg atc gcc tgc ccc atc	192
Lys Arg Ile Arg Ala Glu Ile Val Ala Ser Leu Ile Ala Cys Pro Ile	
50 55 60	
tac gcc ctg ccg gcg gcc ctg gtg ctg gag ctg tgg aag cgg ggc ggg	240
Tyr Ala Leu Pro Ala Ala Leu Val Leu Glu Leu Trp Lys Arg Gly Gly	
65 70 75 80	
acg gcg atc tac agc gat ccc gac gcc tgg ccc ctg tgg tgg ctg ccg	288
Thr Ala Ile Tyr Ser Asp Pro Asp Ala Trp Pro Leu Trp Trp Leu Pro	
85 90 95	
gtc agt ctg atc gtc tat ctg ctg gcg cac gac gcc ttc tac tac tgg	336
Val Ser Leu Ile Val Tyr Leu Leu Ala His Asp Ala Phe Tyr Tyr Trp	
100 105 110	
gtg cac agg gcc ctg cat cac ccg cgc gtc ttc ggc tgg gcc cat gcc	384
Val His Arg Ala Leu His His Pro Arg Val Phe Gly Trp Ala His Ala	
115 120 125	
gaa cac cac cgg tcg cgc gac ccc agc gcc ttc gcc tcc ttc gcc ttc	432
Glu His His Arg Ser Arg Asp Pro Ser Ala Phe Ala Ser Phe Ala Phe	
130 135 140	
gac ccg gcc gag gct gcg gcc acc gcc tgg ttc ctg ccc gcc ctg gcc	480
Asp Pro Ala Glu Ala Ala Ala Thr Ala Trp Phe Leu Pro Ala Leu Ala	
145 150 155 160	
ctg atc gtg ccg atc cac tgg ggc gtg gcc ctg acc ctg ctg acg ctg	528
Leu Ile Val Pro Ile His Trp Gly Val Ala Leu Thr Leu Leu Thr Leu	
165 170 175	
atg tcg ctg acg gcc gcc ctg aac cat gcg ggg cgc gag gtc tgg ccc	576
Met Ser Leu Thr Ala Ala Leu Asn His Ala Gly Arg Glu Val Trp Pro	
180 185 190	
gcc gcc tgg ctg gag cgg gcg ccg ctt cgc tgg ctg atc acc gcc acc	624
Ala Ala Trp Leu Glu Arg Ala Pro Leu Arg Trp Leu Ile Thr Ala Thr	
195 200 205	
cac cac gac gcc cac cac aag cgg ttc aac gga aac tac ggc ctc tat	672
His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly Leu Tyr	
210 215 220	
ttc cag ttc tgg gac cgc tgg gcc ggg act gag gtt tcg gcc gcc ccc	720
Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala Ala Pro	
225 230 235 240	
tcg cca cca tcc ccg gtc atc cct cca gag cgg ccc tca gcg cct ctt	768
Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala Pro Leu	
245 250 255	
cgg tga	774
Arg	

<210> 4  
 <211> 257  
 <212> PRT  
 <213> Brevundimonas sp.

<400> 4  
 Met Leu Arg Asp Leu Leu Ile Thr Thr Leu Ala Leu Ser Leu Ile Ile  
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 Gly Leu Arg Tyr Leu Leu Val Gly Ala Ala Ala His Gly Leu Leu Trp  
                   20                  25                  30  
 Ala Gly Ala Gly Arg Gly Arg Ala Leu Asn Leu Arg Pro Pro Ala Met  
                   35                  40                  45  
 Lys Arg Ile Arg Ala Glu Ile Val Ala Ser Leu Ile Ala Cys Pro Ile  
   50                  55                  60  
 Tyr Ala Leu Pro Ala Ala Leu Val Leu Glu Leu Trp Lys Arg Gly Gly  
   65                  70                  75                  80  
 Thr Ala Ile Tyr Ser Asp Pro Asp Ala Trp Pro Leu Trp Trp Leu Pro  
                   85                  90                  95  
 Val Ser Leu Ile Val Tyr Leu Leu Ala His Asp Ala Phe Tyr Tyr Trp  
                   100                  105                  110  
 Val His Arg Ala Leu His His Pro Arg Val Phe Gly Trp Ala His Ala  
                   115                  120                  125  
 Glu His His Arg Ser Arg Asp Pro Ser Ala Phe Ala Ser Phe Ala Phe  
   130                  135                  140  
 Asp Pro Ala Glu Ala Ala Ala Thr Ala Trp Phe Leu Pro Ala Leu Ala  
   145                  150                  155                  160  
 Leu Ile Val Pro Ile His Trp Gly Val Ala Leu Thr Leu Leu Thr Leu  
                   165                  170                  175  
 Met Ser Leu Thr Ala Ala Leu Asn His Ala Gly Arg Glu Val Trp Pro  
                   180                  185                  190  
 Ala Ala Trp Leu Glu Arg Ala Pro Leu Arg Trp Leu Ile Thr Ala Thr  
                   195                  200                  205  
 His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly Leu Tyr  
   210                  215                  220  
 Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala Ala Pro  
   225                  230                  235                  240  
 Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala Pro Leu  
                   245                  250                  255  
 Arg

<210> 5  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic primer  
  
 <400> 5  
 tacgaattcg atgccctcg ccctg 25  
  
 <210> 6  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic primer  
  
 <400> 6  
 tagaggatcc tcaaggagtg aactggatcg ta 32  
  
 <210> 7  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic primer  
  
 <400> 7  
 tacgaattcg atgaccgccg ccgtcg 26  
  
 <210> 8  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic primer  
  
 <400> 8  
 tagaggatcc tcaagactcg ccgcgccaca a 31  
  
 <210> 9  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 9  
tacgaattcg ctgtcgcgga tgcaggc 27

<210> 10  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 10  
tagaggatcc tgcggttcag cagccgataa aa 32

<210> 11  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 11  
tacgaattcg atgcgagcag cagtgatcgg a 31

<210> 12  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 12  
tagaggatcc aagctcttgg agccctgct 29

<210> 13  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 13  
tacgaattcg atgagcgacg ccgtcct 27

<210> 14  
<211> 29  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 14  
tagaggatcc tcagatgtgg gtccacagg 29

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 15  
tacgaattcg atgatggcgg tggcgggc 28

<210> 16  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 16  
tagaggatcc cccacatctg acggcgct 28

<210> 17  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 17  
tacgaattcg atgtccttca tctcttccgg c 31

<210> 18  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 18  
tagaggatcc accgccatca tgacgagg 28

<210> 19  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic primer  
  
 <400> 19  
 tacgaattcg atggcgatcg tcggttaa 29  
  
 <210> 20  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic primer  
  
 <400> 20  
 tagaggatcc ctagcgtcca agttcggcct 30  
  
 <210> 21  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic primer  
  
 <400> 21  
 tacgaattcg atgcccaccc ccgacgacg 29  
  
 <210> 22  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic primer  
  
 <400> 22  
 tagaggatcc tcagaagcgg ggctcttcca 30  
  
 <210> 23  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic primer  
  
 <400> 23

tacgaattcg atggcctggc tgacgtggat 30

<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 24

tagaggatcc tcaggcgccg ctgctggaa 29

<210> 25

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 25

tacgaattcg atgttgaggg atctgctcat ca 32

<210> 26

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 26

tagaggatcc tcaccgaaga ggcgctgag 29

<210> 27

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 27

tacgaattcg atgctgaaac ggctgggtt 29

<210> 28

<211> 31

<212> DNA

<213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: Synthetic primer

<400> 28

tagaggatcc ctatttccag ttctgggacc g

31

<210> 29

<211> 486

<212> DNA

<213> Brevundimonas sp.

<220>

<221> CDS

<222> (1)..(483)

<400> 29

atg gcc tgg ctg acg tgg atc gcg ctg ttc ctg acc gcc ttt ttg ggc	48
Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly	
1 5 10 15	

atg gag gcg ttc gcc tgg atc atg cac cgc tat gtg atg cac ggt ttc	96
Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe	
20 25 30	

ctg tgg tcc tgg cac cgc agc cat cat gag ccg cac gat cac ccc ctg	144
Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu	
35 40 45	

gag aag aac gac ctg ttc gcc gtg gtc ttc gcc gcc ccg gcc atc gtc	192
Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val	
50 55 60	

atg gtg gcc gtg ggt ctg cac ctg tgg ccc tgg gcc ctg ccg gtc ggc	240
Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly	
65 70 75 80	

ctg ggg atc acg gcc tat ggg atg gtc tat ttc ttc ttc cac gac ggc	288
Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe Phe His Asp Gly	
85 90 95	

ctg gtg cac cgg cgg ttc ccg acg ggc ttt tcc ggg cgg tcc ggc ttc	336
Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe	
100 105 110	

tgg acg cgg cgc atc cag gcg cac cgt ctg cat cac gcc gtg cgc acg	384
Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr	
115 120 125	

cgc gaa ggc tgc gtc tcc ttc ggc ttt ctg tgg gtg cgg tcg gcg cgg	432
Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg	
130 135 140	

gcg ctg aag gcc gaa ctg gct cag aag cgg ggc tct tcc agc agc ggc	480
Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Ser Gly	
145 150 155 160	

gcc tga	486
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Ala

<210> 30  
<211> 161  
<212> PRT  
<213> Brevundimonas sp.

<400> 30  
Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly  
1 5 10 15  
Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe  
20 25 30  
Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu  
35 40 45  
Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val  
50 55 60  
Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly  
65 70 75 80  
Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe Phe His Asp Gly  
85 90 95  
Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe  
100 105 110  
Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr  
115 120 125  
Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg  
130 135 140  
Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Ser Gly  
145 150 155 160

Ala

<210> 31  
<211> 897  
<212> DNA  
<213> Brevundimonas sp.

<220>  
<221> CDS  
<222> (1)..(894)

<400> 31  
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Met Ala Ile Val Gly Leu Arg Pro Gln Pro Val Ser Asp Pro Glu Pro  
1 5 10 15

cag tcg ccc gag aat ctg cgt ggc ctg gtg cag gac cgg ctg gcc gag	96
Gln Ser Pro Glu Asn Leu Arg Gly Leu Val Gln Asp Arg Leu Ala Glu	
20 25 30	
acg gcg ccc tca tcg gac ggt ctt tta gcc ctc gcc gcg cgc gag gcc	144
Thr Ala Pro Ser Ser Asp Gly Leu Leu Ala Leu Ala Ala Arg Glu Ala	
35 40 45	
ctg ctg gga ccg ggc aag cgg gtc agg ccg gtc gtg gcc atg ttg gcc	192
Leu Leu Gly Pro Gly Lys Arg Val Arg Pro Val Val Ala Met Leu Ala	
50 55 60	
gcc gcg cac gtc ggc ggg cgg gcc gag gac gcc ctg gat ttc ggt tgc	240
Ala Ala His Val Gly Gly Arg Ala Glu Asp Ala Leu Asp Phe Gly Cys	
65 70 75 80	
gcg gtc gaa atg gcc cat gcc gcc tcc ctg gtt ctg gac gac ctg ccc	288
Ala Val Glu Met Ala His Ala Ala Ser Leu Val Leu Asp Asp Leu Pro	
85 90 95	
tgt atg gat gat gcg gcc ttg cgg cgc ggt cag ccg acc ctg cac cgc	336
Cys Met Asp Asp Ala Ala Leu Arg Arg Gly Gln Pro Thr Leu His Arg	
100 105 110	
cgc cac ggc gag gat gcg gcc gtg ctg gcg gcc gtg gcc ctt ttg aac	384
Arg His Gly Glu Asp Ala Ala Val Leu Ala Ala Val Ala Leu Leu Asn	
115 120 125	
caa tcg acc cgg ctg att ctg caa agc cgg gcg ccg tcg gag gcg cgg	432
Gln Ser Thr Arg Leu Ile Leu Gln Ser Arg Ala Pro Ser Glu Ala Arg	
130 135 140	
ctg ggc gcc ctg gac gat ttg acg cag gcg atc ggc ttc gac ggc ctg	480
Leu Gly Ala Leu Asp Asp Leu Thr Gln Ala Ile Gly Phe Asp Gly Leu	
145 150 155 160	
gcc gag ggc cag atg cgc gat ctg cgc gac gat ccc gtt cag cgc gac	528
Ala Glu Gly Gln Met Arg Asp Leu Arg Asp Asp Pro Val Gln Arg Asp	
165 170 175	
gtg gtc gcc ctg cgt cgg atc aac gat ctg aag acc ggc gcc ctg ttc	576
Val Val Ala Leu Arg Arg Ile Asn Asp Leu Lys Thr Gly Ala Leu Phe	
180 185 190	
gtc gcg gcc gcg cgg ggc ggc ggc cgg atg ggc ggc ggc gat gcg gac	624
Val Ala Ala Ala Arg Gly Gly Gly Arg Met Gly Gly Gly Asp Ala Asp	
195 200 205	
gac ctg gcg cgt ctc gcc gcc ttc ggc gaa gcg gtc ggc ttc gcc ttc	672
Asp Leu Ala Arg Leu Ala Ala Phe Gly Glu Ala Val Gly Phe Ala Phe	
210 215 220	
cag ctt tgc gac gac ctg atg gac gcc tgt tcg acg agc gag gcc ttg	720
Gln Leu Cys Asp Asp Leu Met Asp Ala Cys Ser Thr Ser Glu Ala Leu	
225 230 235 240	
ggc aag gac gtg ggt cag gat cag ggc gtg acc acc ttc gtg gac ctg	768

Gly	Lys	Asp	Val	Gly	Gln	Asp	Gln	Gly	Val	Thr	Thr	Phe	Val	Asp	Leu	
				245					250					255		
tgg	ggc	gaa	ggc	cgg	gtc	cgc	gcc	ggg	gtg	cgc	cag	tca	ctg	gcc	cgg	816
Trp	Gly	Glu	Gly	Arg	Val	Arg	Ala	Gly	Val	Arg	Gln	Ser	Leu	Ala	Arg	
			260					265					270			
gcg	gcc	gag	gcg	gtc	ggg	cac	gac	agc	ccc	ctg	acg	acc	tat	gtc	ctt	864
Ala	Ala	Glu	Ala	Val	Gly	His	Asp	Ser	Pro	Leu	Thr	Thr	Tyr	Val	Leu	
			275				280					285				
cat	ctc	ttc	cgg	cag	gcc	gaa	ctt	gga	cgc	tag						897
His	Leu	Phe	Arg	Gln	Ala	Glu	Leu	Gly	Arg							
		290				295										

<210> 32  
 <211> 298  
 <212> PRT  
 <213> Brevundimonas sp.

<400> 32															
Met	Ala	Ile	Val	Gly	Leu	Arg	Pro	Gln	Pro	Val	Ser	Asp	Pro	Glu	Pro
1				5					10					15	
Gln	Ser	Pro	Glu	Asn	Leu	Arg	Gly	Leu	Val	Gln	Asp	Arg	Leu	Ala	Glu
			20					25					30		
Thr	Ala	Pro	Ser	Ser	Asp	Gly	Leu	Leu	Ala	Leu	Ala	Ala	Arg	Glu	Ala
		35					40					45			
Leu	Leu	Gly	Pro	Gly	Lys	Arg	Val	Arg	Pro	Val	Val	Ala	Met	Leu	Ala
	50					55					60				
Ala	Ala	His	Val	Gly	Gly	Arg	Ala	Glu	Asp	Ala	Leu	Asp	Phe	Gly	Cys
65					70				75						80
Ala	Val	Glu	Met	Ala	His	Ala	Ala	Ser	Leu	Val	Leu	Asp	Asp	Leu	Pro
				85					90					95	
Cys	Met	Asp	Asp	Ala	Ala	Leu	Arg	Arg	Gly	Gln	Pro	Thr	Leu	His	Arg
		100						105					110		
Arg	His	Gly	Glu	Asp	Ala	Ala	Val	Leu	Ala	Ala	Val	Ala	Leu	Leu	Asn
		115					120					125			
Gln	Ser	Thr	Arg	Leu	Ile	Leu	Gln	Ser	Arg	Ala	Pro	Ser	Glu	Ala	Arg
	130					135					140				
Leu	Gly	Ala	Leu	Asp	Asp	Leu	Thr	Gln	Ala	Ile	Gly	Phe	Asp	Gly	Leu
145					150					155					160
Ala	Glu	Gly	Gln	Met	Arg	Asp	Leu	Arg	Asp	Asp	Pro	Val	Gln	Arg	Asp
				165					170					175	
Val	Val	Ala	Leu	Arg	Arg	Ile	Asn	Asp	Leu	Lys	Thr	Gly	Ala	Leu	Phe
			180					185						190	

Val Ala Ala Ala Arg Gly Gly Gly Arg Met Gly Gly Gly Asp Ala Asp  
195 200 205

Asp Leu Ala Arg Leu Ala Ala Phe Gly Glu Ala Val Gly Phe Ala Phe  
210 215 220

Gln Leu Cys Asp Asp Leu Met Asp Ala Cys Ser Thr Ser Glu Ala Leu  
225 230 235 240

Gly Lys Asp Val Gly Gln Asp Gln Gly Val Thr Thr Phe Val Asp Leu  
245 250 255

Trp Gly Glu Gly Arg Val Arg Ala Gly Val Arg Gln Ser Leu Ala Arg  
260 265 270

Ala Ala Glu Ala Val Gly His Asp Ser Pro Leu Thr Thr Tyr Val Leu  
275 280 285

His Leu Phe Arg Gln Ala Glu Leu Gly Arg  
290 295

<210> 33  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 33  
gtccccgagaa ggaggctaga tatgtccgct cacgctttgc 40

<210> 34  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 34  
cggcggccgc ccgggactaa gcggtgtcac ccttggttct 40

<210> 35  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 35  
atgcggccgc ttataaggac agcccgaatg 30

<210> 36  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 36  
cagtcgacat ccttaactga cggcagcgag

30

<210> 37  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<220>  
<221> misc\_feature  
<222> (9)..(9)  
<223> n is I

<220>  
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<222> (12)..(12)  
<223> n is I

<220>  
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<222> (15)..(15)  
<223> n is I

<220>  
<221> misc\_feature  
<222> (18)..(18)  
<223> n is I

<400> 37  
ttygaygcng gnccnacngt

20

<210> 38  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<220>

<221> misc\_feature  
<222> (3)..(3)  
<223> n is I

<220>  
<221> misc\_feature  
<222> (9)..(9)  
<223> n is I

<220>  
<221> misc\_feature  
<222> (12)..(12)  
<223> n is I

<220>  
<221> misc\_feature  
<222> (15)..(15)  
<223> n is I

<220>  
<221> misc\_feature  
<222> (18)..(18)  
<223> n is I

<400> 38  
ccnggrtgng tncngcncc

20